

Figure 1A

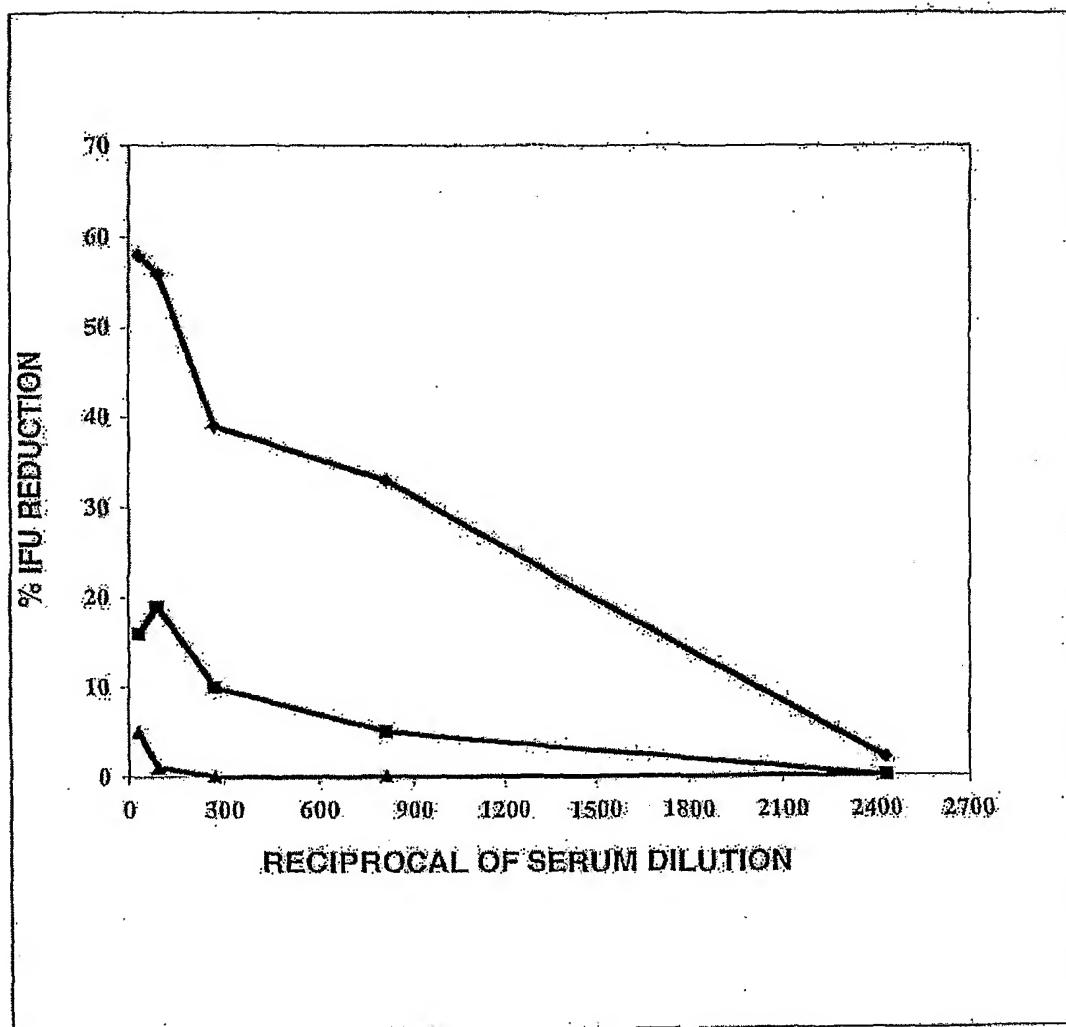
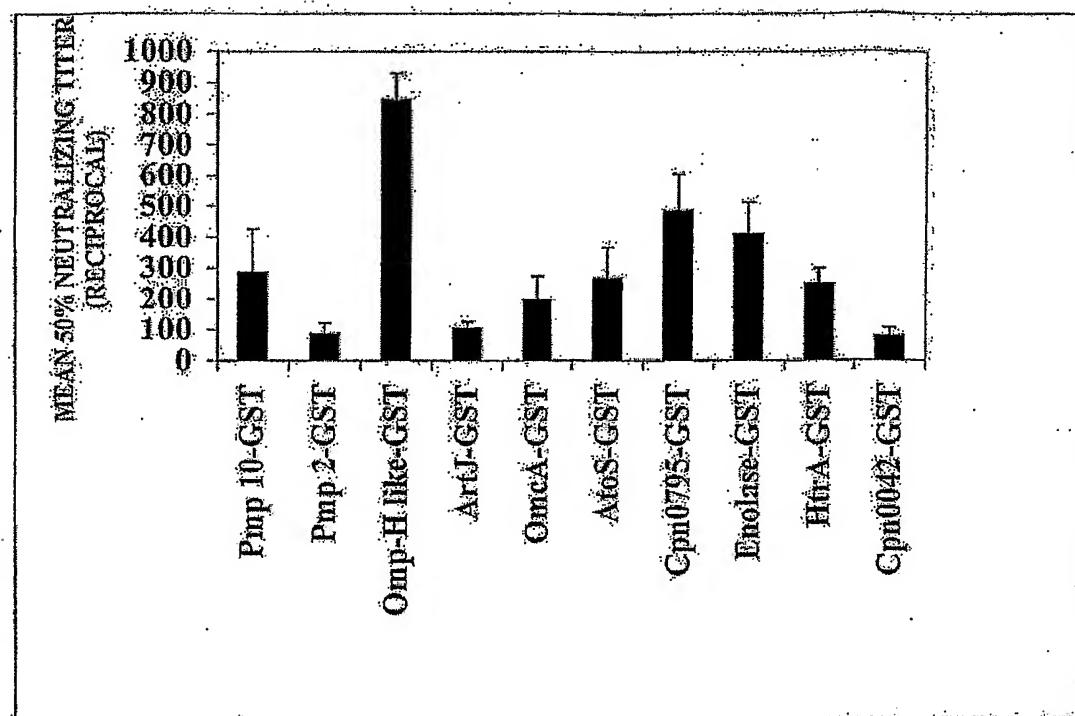


Figure 1B



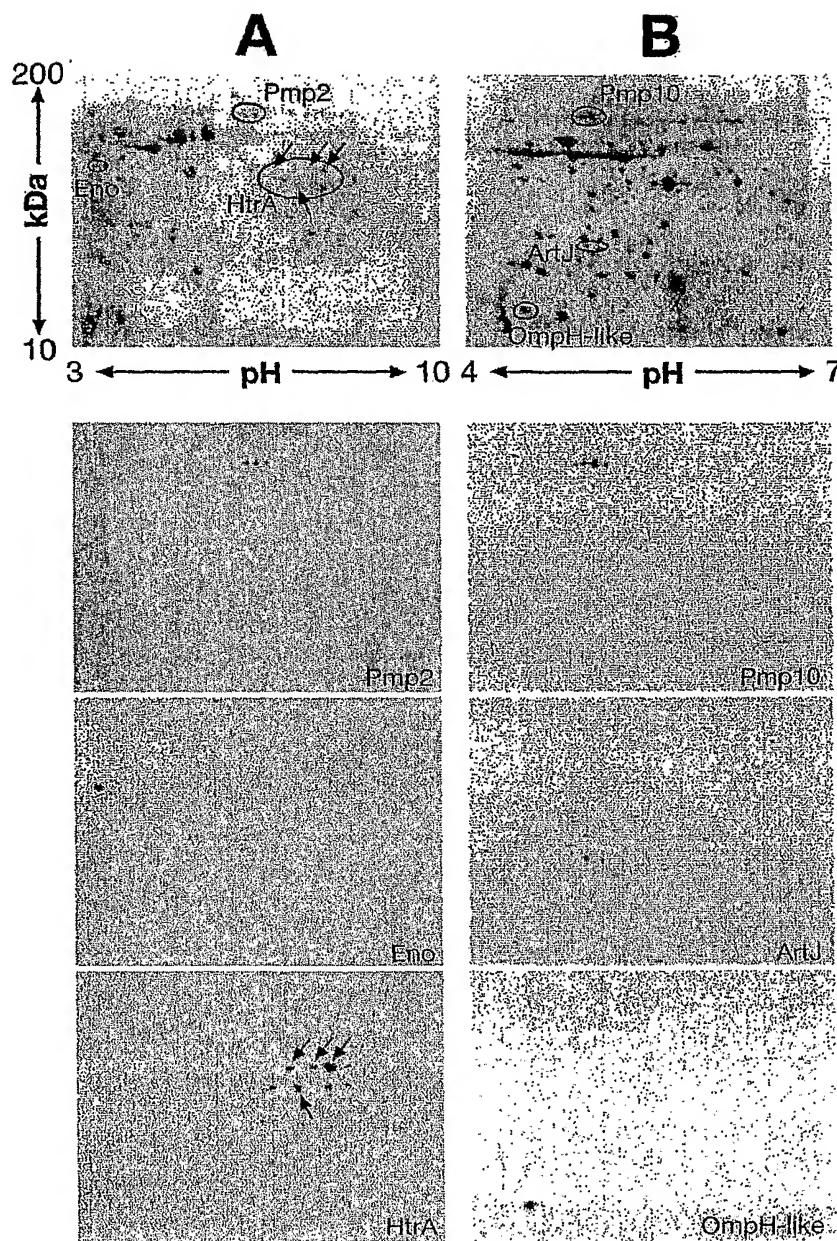


Figure 2

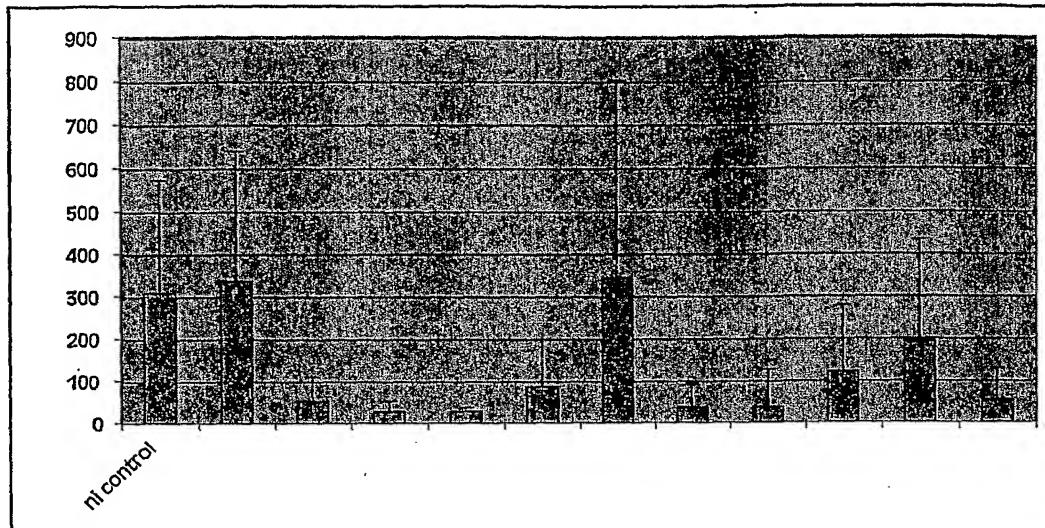


Figure 3. Mean numbers of *C.pneumoniae* IFU recovered from equivalent spleen samples from immunized and mock-immunized hamsters following a systemic challenge. Standard deviation values are shown above the bars. Antigens which induced significant protection are highlighted with an asterisk above the corresponding bar. All antigens were delivered in Freund's adjuvant. n.i. = non immunized controls

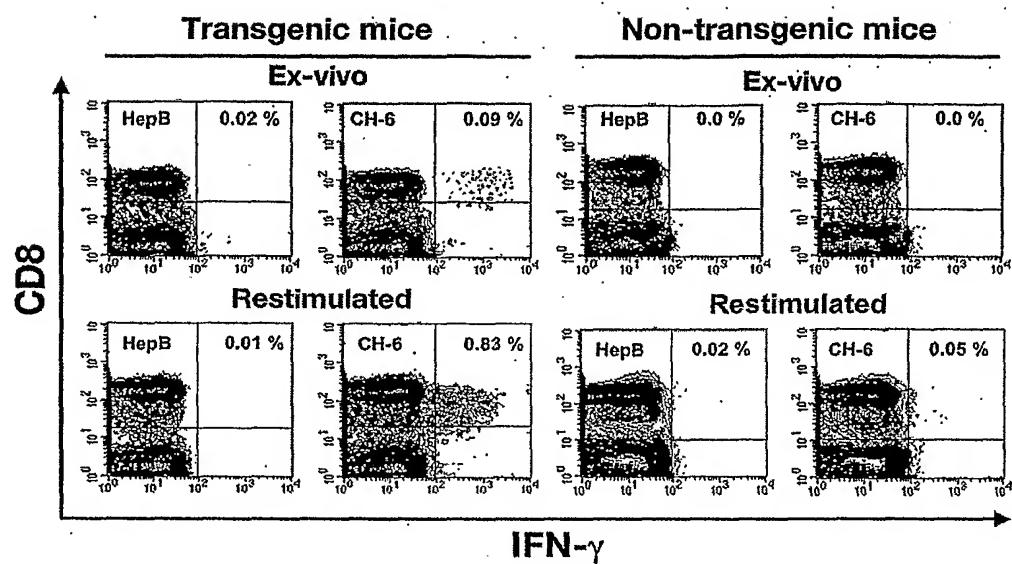
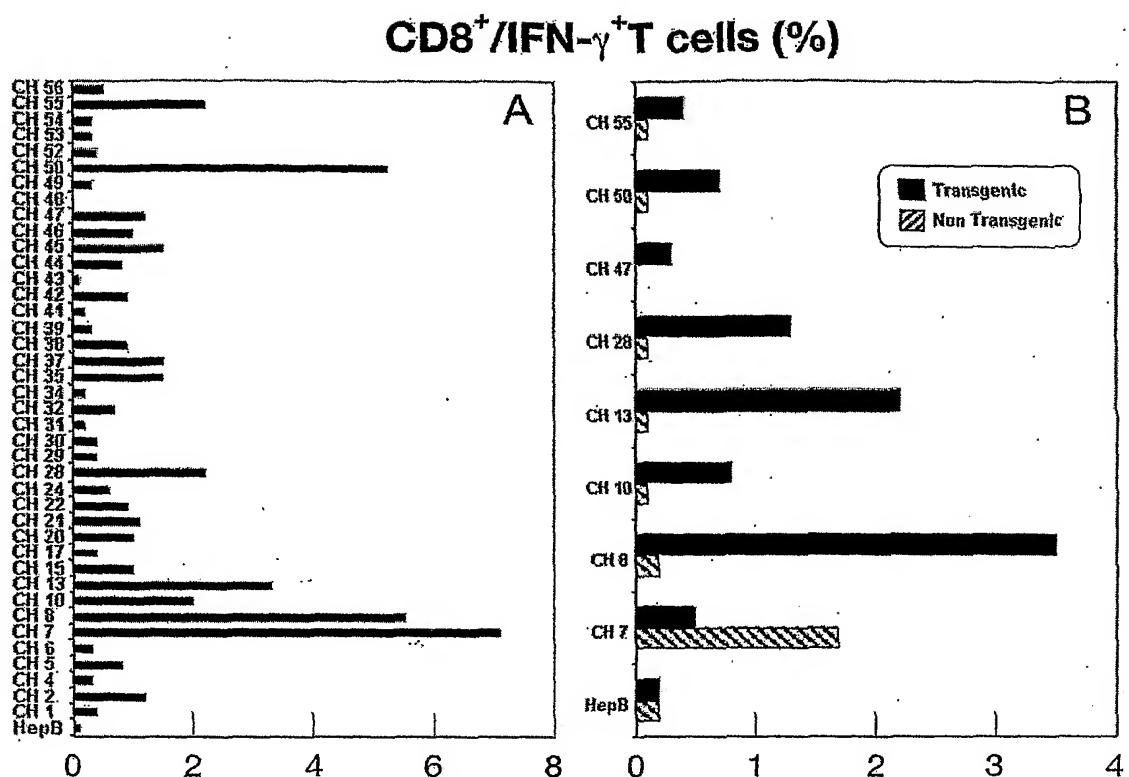
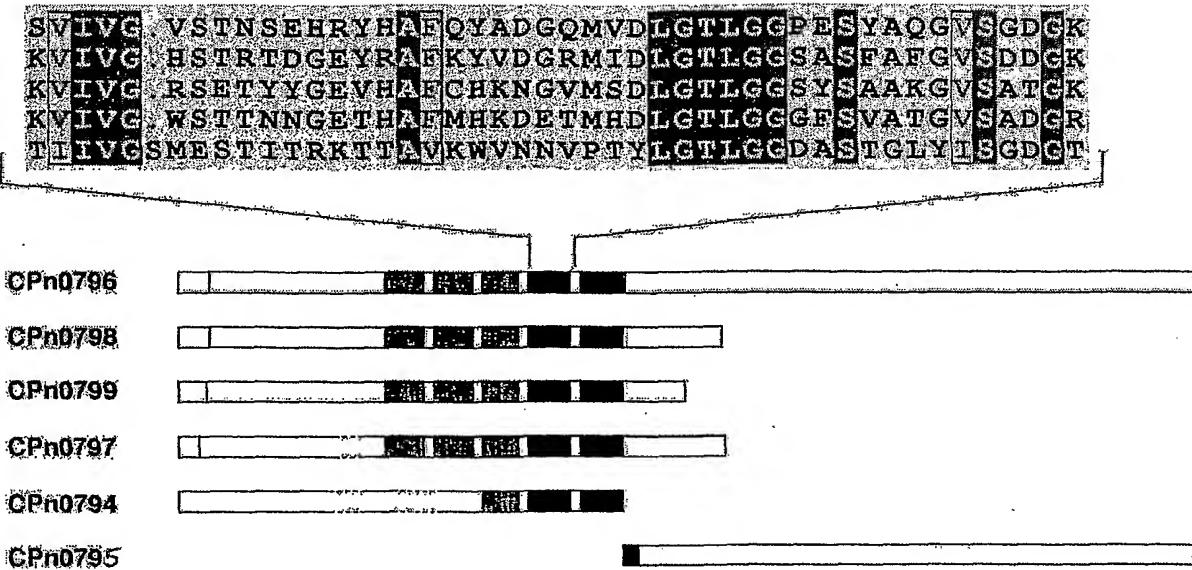
Figure 4

Figure 5





This Alignment shows a new family of proteins expected to constitute a system of antigens probably delivered on the Cpn surface or secreted by a type V (autotransporter) secretion mechanism

Fig. 6

N-terminal alignment

Cpn0796	MQPCLNMSIVRNSALPLPCLSRS	TFKKVRSHMKFMKVLT	WIYRKDLWVTAFL	LTAIPG	60
Cpn0798	-----MKKTCC	QNYRSIGVFS-----	-----VVL	FVLTTQT	27
Cpn0799	-----MAAIKQI	LRSMLSQSSLWMVFL	YCSLSG-----	YCYVITDKP	EDDFHSSSAVK
Cpn0797	-----MSKIKV	LGHLTLC	TLFRGVLC	AAALSN-----	IGYASTSQESPYQKSIED
Cpn0794	-----MSLYQ	KWWNSQLKSLC	YSTVAA-----	-----LIFMIPSQE	32

Cpn0796	SFAHTLVDIAGEPRH	-AAQATGVSGD	GK	-----MKVPDDPF	-----TVGFQYIDGHLQPLEAVR	119	
Cpn0798	LFAGHFIDIG	-TSGL	-YSWARGVSGD	GRVYEGGN-----	-----KYVDGEKF	LLLEGIV	78
Cpn0799	WDHWGKTTLSRL	SNK-KASA	AKAVSG	GATT-----FIKDTWSRTY	-----RNWNYWGT	KELPTSSWV	108
Cpn0797	WKGYTFTDLELLS	KEGWSEAHAVSGNG	SRV-----ASGAGQGSV	-----IWESHLIK	-----	-----	103
Cpn0794	SFADSLIDLNGLDP-----	-----	-----	-----	-----	-----	62

Cpn0796	PQCSVYPNGITPDGT	WVGTNYAIGMGSV	-----K	WVNGK	SE-----PMLPD	TLD-----SVASAV	SADGR	179	
Cpn0798	PRSEALVFKASYDGS	V	-----G	SV	-----I	SEGMQ-----SFAEGV	VSSDGK	137	
Cpn0799	KKS-----KATGISS	SDGS	-----S	-----I	-----V	-----SKAYGI	SSDGK	165	
Cpn0797	-----EASSAEGISKDGE	-----V	-----G	-----W	-----P	-----ATYS-----VARGV	VSGDGS	162	
Cpn0794	-----SVECLSGDGA	-----F	-----V	-----Y	-----Q	-----P	-----F	-----YDGT	107

Cpn0796	-----G	GNRNINL	GAS-----V	-----K	WEDD-VITQLP	SLPDAM	-NACVNG	-----S	-----DGSIT	-----V	-----G	-----IMVDV	233	
Cpn0798	-----T	LYSDDTETN	-----F	-----K	-----WDET	-GMVLPNL	PEDR	-HSCAWDASE	-----DGS	-----V	-----G	-----DAMGS	192	
Cpn0799	-----V	YGS-AKDAWSRT	-----F	-----K	-----WTIGH	-EAQVLP	-VGWAV	-KSVANSV	SANG	-----S	-----T	-----G	-----SVQDA	218
Cpn0797	-----T	VSATARGEDY	-----G	-----W	-----QWQV	GVVKWEKG	-KIKQLKLL	PQGL	-WSEANAI	-----S	-----G	-----T	-----ERGEIS	220
Cpn0794	-----T	TCISLGAGKYN	-----G	-----A	-----GAKWSAD	-----V	-----T	-----PLT	-----G	-----G	-----T	-----S	-----FSYDA	163

Cpn0796	SWRN	-----QWIG	-----DQLSV	-----TT	-----SVASA	-----I	-----SDGT	-----V	-----G	-----SE	-----NAD	-----S	-----T	-----AYKN	288					
Cpn0798	EEIAK	-----YWKD	-----GEQHL	-----SN	-----P	-----A	-----KR	-----SSAHAV	-----SKPGF	-----IV	-----GEFI	-----SE	-----NEV	-----VYHN	248					
Cpn0799	SGILY	-----KWE	-----G	-----NT	-----T	-----H	-----Y	-----S	-----AIAKAV	-----S	-----NGKV	-----IV	-----GRSE	-----TYYGEV	273					
Cpn0797	RNHIV	-----KWNK	-----NAV	-----Y	-----S	-----V	-----S	-----ASAA	-----I	-----S	-----ANGKV	-----IV	-----GWST	-----TNNGET	275					
Cpn0794	SGQPK	-----QWASGATT	-----V	-----T	-----Q	-----A	-----D	-----S	-----GSRSSY	-----A	-----Y	-----A	-----IS	-----DDGT	-----V	-----G	-----MESTITR	-----KTT	-----KWVN	223

Cpn0796	-----G	-----V	-----Y	-----F	-----Y	-----S	-----LAHAV	-----S	-----DGS	-----V	-----G	-----C	-----V	-----G	-----SE	-----HRY	-----QYADGQ	-----V	-----G	-----G	-----343
Cpn0798	-----G	-----V	-----Y	-----F	-----Y	-----S	-----Y	-----S	-----Y	-----V	-----G	-----C	-----V	-----G	-----S	-----Y	-----VYDGR	-----I	-----G	-----G	-----303
Cpn0799	-----G	-----V	-----Y	-----F	-----Y	-----S	-----Y	-----S	-----Y	-----V	-----G	-----C	-----V	-----G	-----S	-----Y	-----VYGG	-----I	-----G	-----G	-----328
Cpn0797	-----G	-----V	-----Y	-----F	-----Y	-----S	-----Y	-----S	-----Y	-----V	-----G	-----C	-----V	-----G	-----S	-----Y	-----YAEGE	-----E	-----G	-----G	-----330
Cpn0794	-----G	-----V	-----Y	-----F	-----Y	-----S	-----Y	-----S	-----Y	-----V	-----G	-----C	-----V	-----G	-----S	-----Y	-----YKDNQ	-----K	-----G	-----G	-----277
Cpn0795	-----G	-----V	-----Y	-----F	-----Y	-----S	-----Y	-----S	-----Y	-----V	-----G	-----C	-----V	-----G	-----S	-----Y	-----K	-----G	-----G	-----G	-----343

Cpn0796	-----PESY	-----AQGV	-----SGD	-----KV	-----V	-----G	-----RAQV	-----P	-----SGDW	-----LCPF	-----QAP	-----SP	-----APV	-----HGG	-----ST	-----VVT	-----S	-----QNP	-----RGM	-----VDIN	403
Cpn0798	SASF	-----AFGV	-----SDDG	-----K	-----V	-----G	-----KFET	-----ELGEC	-----V	-----YLDD	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----337
Cpn0799	KEAC	-----ANAV	-----SIDGE	-----T	-----V	-----G	-----VQSE	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----349
Cpn0797	EEAR	-----VFD	-----ISSEG	-----ND	-----T	-----G	-----SIKTD	-----AGA	-----RAYLF	-----HIHK	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----365
Cpn0795	TSSTAK	-----TVSP	-----DG	-----K	-----V	-----M	-----GRSQI	-----ADG	-----S	-----W	-----MC	-----HTDF	-----SS	-----NN	-----V	-----L	-----FD	-----LDN	-----	-----	-----

FIG. 7

Cpn0796

1	MKF MKVLTPW	IYRKDLWVTA	FLLTAIPGSF	<u>AHTLVDIA</u>		TGV
51	SGDGKIVIGM	KVPDDPFAIT	VGFQYIDGHL	QPL EAVRPQC	SVY PNGITPD	
101	GTVIVGTYA	IGMGSVAVKW	VNGKVSELP M	LPDTLDSVAS	AVSADGRVIG	
151	GNR NINLGA S	VAVKWE DDVI	TQ LPSL PDAM	NAC VNGI SSD	GSII VGT MVD	
201	VSWRNTAVQW	IGDOL SVIGT	LGGTT SVASA	I STDGTVI VG	GSENAD S QTH	
251	AYAYKNGVMS	DIGTLGGFYS	LAHAVSSDGS	VIVGVSTNSE	HRYHAFOYAD	
301	GQMVDLGT LG	GPESY A QGVS	GDGKVIVGRA	QVPSGDWHA F	LGPFQAPSPA	
351	PVHGGSTVVT	SQN P RGMV DI	NATYSSLKNS	QQQLQRLLIQ	HSAKVESVSS	
401	GAPSFTSVKG	AISKOSPAVO	NDVQKGTF LS	YRSOVHGNVQ	NOQLLTGA FM	
451	DWK L ASAPKC	GFKVALHYGS	ODALVERA AL	PYTEQGLGSS	VLSGF GGOVQ	
501	GRYDFNLGET	VVIQPFMGIQ	VLHLSREGYS	EKNVRFPVSY	DSVAYSAATS	
551	FMGAHVFASL	SPKMSTAATL	GVERD LNSHI	DEFKG SVSAM	GNFVLENSTV	
601	SVLRPFASLA	MY YDVRQ QQL	VTLSVVMNQQ	PLTGTLSLVS	QSSY NLSF	

Leader peptide 1-31

Or, alternatively:

Leader peptide 2

b-propeller domain 32-342

or, alternatively:

b-propeller domains

linker region 343-364

helix 365-385

beta barrel 386-648

FIG. 8

Alignment of the C-terminal (beta barrel) domains of the proteins encoded by the *C.pneumoniae* genes Cpn0795 (7016) and Cpn0796 (7107)

7106	-----	TSSTAKTVSPDGKVIMGRSQIADGSWHAFMCHTDFFSSNNVLFDLDN
7107	YADGQ	PESYAQGVSGDGKVIVGRAQVPSGDWHAFLCPFQAPSPAPVHGGST
* * * * * . . * : * * * * * : * : * . * * * * : * : * : * : * : * :		
7106	TYKTLRENGRQLNSIFNLQNMMQLQRASDHEFTTEFGRSNIALGAGLYVNALQNLPSNLAAQ	
7107	VVTSQ--NPRGMVDINATYSSLKNSQQQLQRLLTQHSAKVESVSSGAPSFTSVKGAIISKQ	
. . : . * * : * . . : : : : : * : : : : : * . . : * . . :		
7106	YFGIAKYKIRPKYRLGVFLDHNFSSHVPNNFNVSHNRLWMGAFIGWQDSDLGSSVKVSFG	
7107	SP----AVQNDVQKGTFILSYRSQVHG---NVQNQQLLTGAFMDWKLASAPKCGFKVALH	
. : : : . : * . * . . * * * * * :		
7106	YGKQKATITREQLENTHAGSGESHFEGVAAQIEGRYGRKSLGGHVRFVQPFLGLQFVHTRK	
7107	YGSQDALVERAALPYTEQGLGSSVLSGFGGQVQGRYDFNLGETVVLQPFMGTQVLHLSRE	
..** : * * . * * * . * : * * * * :		
7106	EVTENAVQFPVHYDPIDYSTGVVYLGIGSHIALVDSLHEVGTRMGMEQNFAAHTDRFSGSI	
7107	GYSEKNRFPVSYDSVAYSAATSFMGAHVFAASLSPKMSATAATLGVERDLNHSIDEFKGSV	
:. : * : * * . : * : * . . : * . . : . : * : * : * : * :		
7106	ASIGNFVFEKLDVTHTRAFAEMRVNYELEPYLQSLNLLRVNQQPLQGVGMGFSSDLRYALG	
7107	SAMGNFVLENSTVSVLRPFASLAMYYDVRQQQLVTLSVVMNQQPLTGTLSLVSQSSYNL	
: : * * * : * : * : * * * * :		
7106	F	
7107	F	
* .		

FIG. 9